



Sequences producing significant alignments:

	Score (bits)	E Value	
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<u>gi 21536376 ref NP_005493.2 </u>	ATP-binding cassette, sub-fami...	657	0.0	L
<u>gi 13876613 gb AAK43526.1 </u>	ATP-binding cassette 1 sub-famil...	657	0.0	L
<u>gi 5734135 gb AAD49852.1 </u>	ATP cassette binding transporter ...	657	0.0	L
<u>gi 9755159 gb AAF98175.1 </u>	ATP-binding cassette transporter ...	657	0.0	L
<u>gi 13123945 sp O95477 ABC1_HUMAN</u>	ATP-binding cassette, sub-...	647	0.0	L
<u>gi 4128033 emb CAA10005.1 </u>	ATP-binding cassette transporter...	647	0.0	L
<u>gi 9247086 gb AAF86276.1 </u>	ABCA1 [Homo sapiens]	646	0.0	L
<u>gi 13124694 sp P41233 ABC1_MOUSE</u>	ATP-binding cassette, sub-...	593	e-168	L
<u>gi 1082238 pir A54774</u>	ATP binding cassette transporter ABC...	593	e-168	L
<u>gi 11611825 gb AAG39073.1 </u>	ATP-binding cassette 1, sub-fami...	593	e-168	L
<u>gi 34577069 ref NP_038482.2 </u>	ATP-binding cassette 1, sub-fa...	593	e-168	L
<u>gi 30017417 ref NP_835196.1 </u>	ATP-binding cassette, sub-fami...	587	e-166	L
<u>gi 45383826 ref NP_989476.1 </u>	ATP-binding cassette, sub-fami...	476	e-133	L
<u>gi 47220000 emb CAG11533.1 </u>	unnamed protein product [Tetrao...	304	2e-81	
<u>gi 47212013 emb CAF95419.1 </u>	unnamed protein product [Tetrao...	300	4e-80	

gi 47211165 emb CAF95992.1 	unnamed protein product [Tetrao...]	264	4e-69	
gi 27806343 ref NP_776646.1 	ATP-binding cassette, sub-fami...	185	1e-45	
gi 34859941 ref XP_241525.2 	similar to ATP-binding casset...	183	5e-45	
gi 6671495 ref NP_031404.1 	ATP-binding cassette, sub-famil...	179	1e-43	
gi 47219577 emb CAG02283.1 	unnamed protein product [Tetrao...]	169	1e-40	
gi 2959643 qb AAC05632.1 	rim ABC transporter [Homo sapiens]	149	9e-35	
gi 6707663 sp P78363 ABCR_HUMAN	Retinal-specific ATP-bindin...	148	2e-34	
gi 4557876 ref NP_000341.1 	ATP-binding cassette, sub-famil...	148	2e-34	
gi 2969966 emb CAA75729.1 	ABCR [Homo sapiens]	148	2e-34	
gi 3243082 qb AAC23915.1 	ATP-binding cassette transporter ...	148	2e-34	
gi 40556959 gb AAR87836.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 40556955 gb AAR87834.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 40556957 gb AAR87835.1 	ABCA4 [Canis familiaris]	147	4e-34	
gi 47223059 emb CAG07146.1 	unnamed protein product [Tetrao...]	132	1e-29	
gi 47225166 emb CAF98793.1 	unnamed protein product [Tetrao...]	131	3e-29	
gi 34862327 ref XP_216829.2 	similar to ATP-binding casset...	127	4e-28	
gi 46485412 ref NP_997481.1 	ATP-binding cassette, sub-fami...	127	4e-28	
gi 15451840 ref NP_038878.1 	ATP-binding cassette, sub-fami...	127	7e-28	
gi 15451838 ref NP_150651.1 	ATP-binding cassette, sub-fami...	98	5e-19	
gi 9506365 ref NP_061985.1 	ATP-binding cassette, sub-famil...	98	5e-19	
gi 22725156 gb AAN04657.1 	ABC transporter ABCA7 [Homo sapi...	98	5e-19	
gi 12656651 gb AAK00959.1 	ABC transporter member 7 [Homo s...	98	5e-19	
gi 46139435 ref XP_391408.1 	hypothetical protein FG11232.1...	36	1.5	
gi 45446740 ref NP_001597.2 	ATP-binding cassette, sub-fami...	35	2.7	
gi 1082239 pir B54774	ATP binding cassette transporter ABC...	35	2.7	
gi 47078218 ref NP_997698.1 	ATP-binding cassette, sub-fami...	35	2.7	
gi 9957467 gb AAG09372.1 	ATP-binding cassette sub-family A...	35	2.7	
gi 11346269 pir A59189	ATP-binding cassette transporter - ...	35	2.7	
gi 11993939 ref NP_031405.1 	ATP-binding cassette, sub-fami...	35	2.7	
gi 14916523 sp Q9BZC7 ABC2_HUMAN	ATP-binding cassette, sub-...	35	2.7	
gi 13242308 ref NP_077372.1 	ATP-binding cassette, sub-fami...	35	2.7	
gi 47209044 emb CAF91746.1 	unnamed protein product [Tetrao...]	35	3.6	
gi 14250599 gb AAH08755.1 	ABCA2 protein [Homo sapiens]	35	3.6	
gi 47212140 emb CAF95654.1 	unnamed protein product [Tetrao...]	34	8.7	
gi 42491191 emb CAF25489.1 	HuD protein [Listonella anguil...	34	8.7	
gi 13475669 ref NP_107236.1 	3-hydroxybutyryl-coA dehydroge...	33	12	
gi 48846428 ref ZP_00300691.1 	COG1283: Na+/phosphate sympo...	33	16	
gi 21430570 gb AAM50963.1 	RE06730p [Drosophila melanogaster]	33	16	
gi 33519597 ref NP_878429.1 	carbamoyl-phosphate synthase l...	33	16	
gi 24648559 ref NP_650925.1 	CG3822-PA [Drosophila melanoga...	33	16	
gi 50294708 ref XP_449765.1 	unnamed protein product [Candi...	33	16	
gi 47215635 emb CAG01352.1 	unnamed protein product [Tetrao...]	32	21	
gi 2631999 emb CAA05373.1 	MviN protein [Vibrio cholerae]	32	28	
gi 15640699 ref NP_230329.1 	MviN protein [Vibrio cholerae ...]	32	28	
gi 21428506 gb AAM49913.1 	LD28992p [Drosophila melanogaster]	32	28	
gi 28379892 ref NP_786784.1 	ATP-dependent Clp protease, AT...	32	28	
gi 48102288 ref XP_395322.1 	similar to CG3999-PA [Apis mel...	32	28	
gi 39583220 emb CAE61438.1 	Hypothetical protein CBG05321 [...]	32	28	
gi 49072300 ref XP_400439.1 	hypothetical protein UM02824.1...	32	28	
gi 23577904 ref NP_703103.1 	unknown [Rachiplusia ou multip...	32	28	
gi 16769402 gb AAL28920.1 	LD29423p [Drosophila melanogaster]	32	28	

<u>gi 24639632 ref NP_572152.2 </u>	CG4857-PB [Drosophila melanogaster] ...	<u>32</u>	28	<input checked="" type="checkbox"/> L
<u>gi 28897306 ref NP_796911.1 </u>	MviN protein [Vibrio parahaemolyticus] ...	<u>32</u>	28	
<u>gi 32405532 ref XP_323379.1 </u>	predicted protein [Neurospora crassa] ...	<u>32</u>	28	
<u>gi 4185888 emb CAA21827.1 </u>	EG:EG0007.4 [Drosophila melanogaster] ...	<u>32</u>	28	
<u>gi 50290817 ref XP_447841.1 </u>	unnamed protein product [Candida rugosa] ...	<u>32</u>	28	
<u>gi 22788744 ref NP_690455.1 </u>	DNA ligase III [Heliothis zea] ...	<u>32</u>	28	
<u>gi 15894929 ref NP_348278.1 </u>	Aspartate ammonia-lyase [Clostridium perfringens] ...	<u>32</u>	38	
<u>gi 46121537 ref XP_385323.1 </u>	hypothetical protein FG05147.1... [Yersinia pestis] ...	<u>32</u>	38	
<u>gi 48104558 ref XP_395803.1 </u>	similar to ENSANGP00000016433 ...	<u>32</u>	38	<input checked="" type="checkbox"/> L
<u>gi 20806867 ref NP_622038.1 </u>	ABC-type dipeptide/oligopeptidase [S. cerevisiae] ...	<u>31</u>	51	
<u>gi 16765904 ref NP_461519.1 </u>	leucine-rich repeat protein [Pseudomonas aeruginosa] ...	<u>31</u>	51	
<u>gi 45361665 ref NP_989410.1 </u>	hypothetical protein MGC76219 ...	<u>31</u>	51	<input checked="" type="checkbox"/> L
<u>gi 39996841 ref NP_952792.1 </u>	Na/Pi-cotransporter family protein [Escherichia coli] ...	<u>31</u>	51	
<u>gi 39998079 ref NP_954030.1 </u>	conserved hypothetical protein [Mycobacterium tuberculosis] ...	<u>31</u>	51	
<u>gi 9049789 gb AAF82481.1 </u>	leucine-rich repeat protein [phagocytosis-related protein] ...	<u>31</u>	51	
<u>gi 21243605 ref NP_643187.1 </u>	conserved hypothetical protein [Mycobacterium tuberculosis] ...	<u>31</u>	51	
<u>gi 41408181 ref NP_961017.1 </u>	hypothetical protein MAP2083c ...	<u>31</u>	51	
<u>gi 49903552 gb AAH76991.1 </u>	MGC76219 protein [Xenopus tropicalis] ...	<u>31</u>	51	<input checked="" type="checkbox"/> L
<u>gi 34896534 ref NP_909611.1 </u>	putative retrotransposon gag protein [S. pombe] ...	<u>31</u>	51	
<u>gi 31544841 ref NP_853419.1 </u>	ATP/GTPase [Mycoplasma gallisepticum] ...	<u>31</u>	68	
<u>gi 37181847 gb AAQ88727.1 </u>	JAM-IT/VE-JAM [Homo sapiens]	<u>31</u>	68	
<u>gi 10864029 ref NP_067042.1 </u>	junctional adhesion molecule 2 ...	<u>31</u>	68	<input checked="" type="checkbox"/> L
<u>gi 7109693 gb AAF36764.1 </u>	putative ATP/GTP-binding protein [S. pombe] ...	<u>31</u>	68	
<u>gi 39590633 emb CAE65003.1 </u>	Hypothetical protein CBG09841 [Mycobacterium tuberculosis] ...	<u>31</u>	68	
<u>gi 2492605 sp P97998 MDL1_CANAL</u>	ATP-dependent permease MDL1 ...	<u>31</u>	68	
<u>gi 19110396 gb AAL82538.1 </u>	C21ORF43 [Homo sapiens]	<u>31</u>	68	<input checked="" type="checkbox"/> L
<u>gi 46440040 gb EAK99351.1 </u>	hypothetical protein Ca019.2615 ...	<u>31</u>	68	
<u>gi 39594406 emb CAE71984.1 </u>	Hypothetical protein CBG19059 [Mycobacterium tuberculosis] ...	<u>31</u>	68	
<u>gi 6635285 gb AAF19761.1 </u>	mutant matrix melanosomal protein [Homo sapiens] ...	<u>30</u>	91	<input checked="" type="checkbox"/> L
<u>gi 38076905 ref XP_127911.3 </u>	RIKEN cDNA 2410089E03 [Mus musculus] ...	<u>30</u>	91	<input checked="" type="checkbox"/> L
<u>gi 39580881 emb CAE73879.1 </u>	Hypothetical protein CBG21472 [Mycobacterium tuberculosis] ...	<u>30</u>	91	
<u>gi 38346799 emb CAD41367.2 </u>	OSJNBa0088A01.6 [Oryza sativa (rice)] ...	<u>30</u>	91	
<u>gi 34862223 ref XP_343147.1 </u>	similar to Melanocyte protein [Homo sapiens] ...	<u>30</u>	91	<input checked="" type="checkbox"/> L
<u>gi 49255967 gb AAH71083.1 </u>	Unknown (protein for IMAGE:63160...) ...	<u>30</u>	91	

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

>gi|21536376|ref|NP_005493.2| L ATP-binding cassette, sub-family A member 1; ATP high density lipoprotein deficiency, Tangier type, 1; cholesterol efflux regulatory protein [Homo sapiens]
Length = 2261

Score = 657 bits (1543), Expect = 0.0
Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQWP--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
FGKYPSELQWP EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
Sbjct: 1371 FGKYPSELQWPWMYNEQYTFVSNDAPEDTGTLELLNALT KDPFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD-UKKMLPVCPGAGGLPPQQ-M 114
AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD KKMLPVCPGAGGLPPQQ

Subjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490
 Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE
 Subjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNFRYGGFSLGVSNTQALPPSQE 1550
 Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Subjct: 1551 VNDAIKQMKKKHLKLAKD--SSADRFLNSLGRFMTGLDTKNNVKWWFNNKGWHAISSFLNV 1608
 Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Subjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

>gi|13876613|gb|AAK43526.1| L ATP-binding cassette 1 sub-family A member 1 [Homo
 Length = 2261

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Subjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KDPFGTRCMEGNPIPDTPCQ 1430
 Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD KKMLPVCPPGAGGLPPPQ
 Subjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490
 Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNTQALPPSQE
 Subjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNFRYGGFSLGVSNTQALPPSQE 1550
 Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Subjct: 1551 VNDAIKQMKKKHLKLAKD--SSADRFLNSLGRFMTGLDTKNNVKWWFNNKGWHAISSFLNV 1608
 Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Subjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

>gi|5734135|gb|AAD49852.1| L ATP cassette binding transporter 1 [Homo sapiens]
 Length = 849

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Subjct: 428 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KDPFGTRCMEGNPIPDTPCQ 487
 Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSD KKMLPVCPPGAGGLPPPQ
 Subjct: 488 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 547
 Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU----MNEFRYGGFSLGVSNTQALPPSQE 168

QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNQALPPSQE
 Sbjct: 548 QNTADILQDLTGRNISDYLVKTYYQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 607

Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 608 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNV 665

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 666 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 711

>gi|9755159|gb|AAF98175.1| L ATP-binding cassette transporter 1 [Homo sapiens]
 Length = 2261

Score = 657 bits (1543), Expect = 0.0
 Identities = 237/286 (82%), Positives = 240/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KDPFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYYQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

>gi|13123945|sp|O95477|ABC1_HUMAN L ATP-binding cassette, sub-family A, member 1
 transporter 1) (ATP-binding cassette 1) (ABC-1)
 (Cholesterol efflux regulatory protein)
 Length = 2261

Score = 647 bits (1519), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLELLNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALT KDPFGTRCMEGNPIPDTPCQ 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNQALPPSQE

Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIVWNEFRYGGFSLGVSNQALPPSQE 1550
 Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1551 VNDATKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNV 1608
 Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1654

>gi|4128033|emb|CAA10005.1| **L** ATP-binding cassette transporter-1 (ABC-1) [Homo sapiens]
gi|5734101|gb|AAD49849.1| **L** ATP cassette binding transporter 1 [Homo sapiens]
 Length = 2201

Score = 647 bits (1519), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLLENNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLLENNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1311 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLLENNALT KDPFGTRCMEGNPIPDTPCQ 1370
 Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1371 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD KIKKMLPVCPPGAGGLPPPQRK 1430
 Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1431 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIVWNEFRYGGFSLGVSNQALPPSQE 1490
 Query: 169 -GDAIKQM-UHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1491 VNDATKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNV 1548
 Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTTSVD
 Sbjct: 1549 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1594

>gi|9247086|gb|AAF86276.1| **L** ABCA1 [Homo sapiens]
 Length = 2261

Score = 646 bits (1517), Expect = 0.0
 Identities = 235/286 (82%), Positives = 238/286 (83%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLLENNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPEDTGTLLENNALT PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLLENNALT KDPFGTRCMEGNPIPDTPCQ 1430
 Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD KIKKMLPVCPPGAGGLPPPQRK 1490
 Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 QNTADILQDLTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIVWNEFRYGGFSLGVSNQALPPSQE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DA KQM HL SSAD LNSLG MTGLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAXKQMKKHLKLAKD--SSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSEFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 253
 + AIL NLQKGENPSHYGITAFNHPLNLTQQLSEVA MTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAXMTTSVD 1654

>[gi|13124694|sp|P41233|ABC1_MOUSE](#) **L** ATP-binding cassette, sub-family A, member 1 transporter 1) (ATP-binding cassette 1) (ABC-1)
 Length = 2261

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPED GT ELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDMGTQELLNALTDPFGTRCMEGNPIPDTPC 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWMTMQNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWMT+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWMTKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSN+QALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1491 QKTADILQNLGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1550

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKKLLKLKD--TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSEFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSQYGITAFNHPLNLTQQLSEVALMTTSVD 1654

>[gi|1082238|pir||A54774](#) ATP binding cassette transporter ABC1 - mouse
[gi|495257|emb|CAA53530.1|](#) **L** ABC transporter [Mus musculus]
 Length = 2201

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPED GT ELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELQPWMYNEQYTFVSNDAPEDMGTQELLNALTDPFGTRCMEGNPIPDTPC 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWMTMQNPSPACQCSSD-UKKMLPVCPPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWMT+NPSPACQCSSD KKMLPVCPPGAGGLPPPQ
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWMTKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSN+QALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1431 QKTADILQNLGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1490

Query: 169 -GDAIKQM-UHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210

DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1491 VNDAIKQMKLLKLTKD--TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1548

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1549 INNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1594

>gi|11611825|gb|AAG39073.1| L ATP-binding cassette 1, sub-family A, member 1 [Mu
 Length = 2198

Score = 593 bits (1391), Expect = e-168
 Identities = 219/285 (76%), Positives = 230/285 (80%), Gaps = 35/285 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPED GT ELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELQPWMYNEQYTFVSNDAPEDMGTQELLNALTDPFGTRCMEGNPIPDTPC 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD-UKKMLPVCPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSACQCSD KKMLPVCPGAGGLPPPQ
 Sbjct: 1371 AGEEDWTISPVPQSVIDLFQNGNWTMKNPSPACQCSDKIKKMLPVCPGAGGLPPPQ 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1431 QKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1490

Query: 169 -GDAIKQMUHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 211
 DAIKQM L SAD L+SLG M GLDT KV KG AISSFLNV+
 Sbjct: 1491 VNDAIKQMKLLKLTK--SADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1547

Query: 212 --AILM-NLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 253
 AIL NLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1548 NNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1592

>gi|34577069|ref|NP_038482.2| L ATP-binding cassette 1, sub-family A, member 1;
 1 [Mus musculus]
 Length = 2261

Score = 593 bits (1391), Expect = e-168
 Identities = 219/286 (76%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTFVSNDAPED GT ELLNALT PGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDMGTQELLNALTDPFGTRCMEGNPIPDTPC 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSD-UKKMLPVCPGAGGLPPPQ-M 114
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSACQCSD KKMLPVCPGAGGLPPPQ
 Sbjct: 1431 AGEEDWTISPVPQSVIDLFQNGNWTMKNPSPACQCSDKIKKMLPVCPGAGGLPPPQ 1490

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 Q TADILQ+LTG ISDYLVKT+ QIIAKSL +NEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1491 QKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1550

Query: 169 -GDAIKQMUHL----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQM L +SAD L+SLG M GLDT KV KG AISSFLNV
 Sbjct: 1551 VNDAIKQMKLLKLTK--TSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNV 1608

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTQQLSEVALMTTSVD
 Sbjct: 1609 INNAILRANLQKGENPSQYGITAFNHPLNLTQQLSEVALMTTSVD 1654

>gi|30017417|ref|NP_835196.1| L ATP-binding cassette, sub-family A (ABC1), member norvegicus]
 gi|28912192|gb|AA053557.1| L ATP-binding cassette 1 [Rattus norvegicus]
 Length = 2201

Score = 587 bits (1378), Expect = e-166
 Identities = 217/286 (75%), Positives = 231/286 (80%), Gaps = 35/286 (12%)

Query: 1 FGKYPSELQPW--UEQYTFVSNDAPEDTGTLELLNALT--PGFGTRCMEGNPIPDTPCQ 56
 FGKYP+LELQPW EQYTFVSNDAPED GT ELLNALT PGFGTRCMEGNPIP+TPC
 Sbjct: 1311 FGKYPNLELQPWMYNEQYTFVSNDAPEDMGTQELLNALTDPGFGTRCMEGNPIPNTPCL 1370

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSD-UKKMLPVCPGAGGLPPPQ-M 114
 GEE+WTT PVPQT+MDLFQNGNWTM+NPSP+CQCSSD KKMLPVCPGAGGLPPPQ
 Sbjct: 1371 VGEEDWTTGPVVPQTLMDFQNGNWTMKNPSPSCQCSSDKIKKMLPVCPGAGGLPPPQRK 1430

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 Q TADILQ+LTG SDYLVKT+ QIIAKSL +NEFRYGGFSLGV++QALPPSQE
 Sbjct: 1431 QKTADILQNLGRNNSDYLVKTIVQIIAKSLKNKVWVNEFRYGGFSLGVSDSQALPPSQE 1490

Query: 169 -GDAIKQMUHL-----CASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 +AIKQM L SSAD L+SLG MTGLDT KV KG AISSFLNV
 Sbjct: 1491 VNNAIKQMKLLKLTKD--SSADRFLSSLGRFMTGLDTKNNVKWFNNKGWHAISSFLNV 1548

Query: 211 M--AILM-NLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 253
 + AIL NLQKGENPS YGITAFNHPLNLTQQLSEVALMTTSVD
 Sbjct: 1549 INNAILRANLQKGENPSQYGITAFNHPLNLTQQLSEVALMTTSVD 1594

>gi|45383826|ref|NP_989476.1| L ATP-binding cassette, sub-family A (ABC1), member
 gi|18028983|gb|AAL56247.1| L ATP-binding cassette transporter 1 [Gallus gallus]
 Length = 2260

Score = 476 bits (1115), Expect = e-133
 Identities = 187/286 (65%), Positives = 218/286 (76%), Gaps = 36/286 (12%)

Query: 1 FGKYPSELQPWU-EQYTFVSNDAPEDTGTLELLNAL--TPGFTRCMEGNPIPDTPCQ 56
 FGKYPSELQPW EQYTF+SNDAPED GT +LL+AL PGFGTRCM+G+ IPDTPC
 Sbjct: 1371 FGKYPSELQPWMYDEQYTFISNDAPEDAGTQKLLDALLNKPGFGTRCMQGHSSIPDTPCT 1430

Query: 57 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDU-KKKMLPVCPGAGGLPPPQM- 114
 G++EWTTA VP +++++ + GNW+M+NPSP+C+CS++ KKMLPVCPGAGGLPPPQ
 Sbjct: 1431 VGQKEWTTASVPDSVLEILR-GNWSMENPSPSCECSNEKIKKMLPVCPGAGGLPPPQE 1489

Query: 115 QNTADILQDLTGM-ISDYLVKTW-QIIAKSLU---MNEFRYGGFSLGVSNQALPPSQE 168
 Q+TADILQ+LTG ISDYLVKT+ QII KSL +NEFRYGGFSLG ++ LPPS E
 Sbjct: 1490 QDTADILQNLGRNISDYLVKTVAQIIGKSLKNKIWVNEFRYGGFSLGARSSHVLPPSNE 1549

Query: 169 G-DAIKQ-----MUHLCASSAD--LNSLGU-MTGLDT---YKV---UKG--AISSFLNV 210
 DAIKQ + SS D LN+L M GLDT KV KG AI+SFLNV
 Sbjct: 1550 VTDAIKQVKKILEAQ--GSSGDRFLNNLASFMKGLDTKNNVKWFNNKGWHAIASFLNV 1607

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=> D L3

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TI LXR/RXR activation enhances basolateral efflux of cholesterol in CaCo-2 cells.
AU Murthy Shubha; Born Ella; Mathur Satya N; Field F Jeffrey
CS Department of Veterans Affairs and Department of Internal Medicine,
University of Iowa, Iowa City, IA 52242, USA.. shubha-murthy@uiowa.edu
NC HL49264 (NHLBI)
SO Journal of lipid research, (2002 Jul) 43 (7) 1054-64.
Journal code: 0376606. ISSN: 0022-2275.
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